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     (FILE 'HOME' ENTERED AT 15:06:55 ON 22 NOV 2002)

     FILE 'MEDLINE, EMBASE, BIOSIS, BIOTECHDS, SCISEARCH, HCAPLUS, NTIS,
     LIFESCI' ENTERED AT 15:07:18 ON 22 NOV 2002
L1           149 S SUCROSE(A) PHOSPHOTRANSFERASE?
L2       5695523 S CLON? OR EXPRESS? OR RECOMBINANT
L3            64 S L1 AND L2
L4            31 DUP REM L3 (33 DUPLICATES REMOVED)
                 E POMPEJUS M/AU
L5            28 S E3
L6             0 S L4 AND L5
                 E SCHRODER H/AU
L7          1962 S E3
L8             0 S L4 AND L7
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     (FILE 'HOME' ENTERED AT 15:06:55 ON 22 NOV 2002)

     FILE 'MEDLINE, EMBASE, BIOSIS, BIOTECHDS, SCISEARCH, HCAPLUS, NTIS,
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L1           149 S SUCROSE(A) PHOSPHOTRANSFERASE?
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L5            28 S E3
L6             0 S L4 AND L5
                 E SCHRODER H/AU
L7          1962 S E3
L8             0 S L4 AND L7
                 E KROGER B/AU
L9            93 S E3
L10            0 S L4 AND L9
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NEWS 4 Apr 09 ZDB will be removed from STN
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NEWS 6 Apr 22 Records from IP.com available in CAPLUS, HCAPLUS, and ZCAPLUS
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NEWS 8 Apr 22 Federal Research in Progress (FEDRIP) now available
NEWS 9 Jun 03 New e-mail delivery for search results now available
NEWS 10 Jun 10 MEDLINE Reload
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saved answer sets no longer valid
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NEWS 19 Aug 19 Aquatic Toxicity Information Retrieval (AQUIRE)
now available on STN
NEWS 20 Aug 19 IFIPAT, IFICDB, and IFIUDB have been reloaded
NEWS 21 Aug 19 The MEDLINE file segment of TOXCENTER has been reloaded
NEWS 22 Aug 26 Sequence searching in REGISTRY enhanced
NEWS 23 Sep 03 JAPIO has been reloaded and enhanced
NEWS 24 Sep 16 Experimental properties added to the REGISTRY file
NEWS 25 Sep 16 Indexing added to some pre-1967 records in CA/CAPLUS
NEWS 26 Sep 16 CA Section Thesaurus available in CAPLUS and CA
NEWS 27 Oct 01 CASREACT Enriched with Reactions from 1907 to 1985
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NEWS 30 Oct 24 Nutraceuticals International (NUTRACEUT) now available on STN
NEWS 31 Oct 25 MEDLINE SDI run of October 8, 2002
NEWS 32 Nov 18 DKILIT has been renamed APOLLIT

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=> file medline embase biosis biotechds scisearch hcaplus ntis lifesci

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FULL ESTIMATED COST	0.21	0.21

FILE 'MEDLINE' ENTERED AT 15:07:18 ON 22 NOV 2002

FILE 'EMBASE' ENTERED AT 15:07:18 ON 22 NOV 2002

FILE 'BIOSIS' ENTERED AT 15:07:18 ON 22 NOV 2002

FILE 'BIOTECHDS' ENTERED AT 15:07:18 ON 22 NOV 2002

FILE 'SCISEARCH' ENTERED AT 15:07:18 ON 22 NOV 2002

FILE 'HCAPLUS' ENTERED AT 15:07:18 ON 22 NOV 2002

FILE 'NTIS' ENTERED AT 15:07:18 ON 22 NOV 2002

FILE 'LIFESCI' ENTERED AT 15:07:18 ON 22 NOV 2002


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=> s sucrose(a) phosphotransferase?
L1          149 SUCROSE(A) PHOSPHOTRANSFERASE?

=> s clon? or express? or recombinant
   4 FILES SEARCHED...
L2      5695523 CLON? OR EXPRESS? OR RECOMBINANT

=> s l1 and l2
L3           64 L1 AND L2

=> dup rem l3
PROCESSING COMPLETED FOR L3
L4            31 DUP REM L3 (33 DUPLICATES REMOVED)

=> d 1-31 ibib ab

L4   ANSWER 1 OF 31  HCAPLUS  COPYRIGHT 2002 ACS
ACCESSION NUMBER:         2001:265608  HCAPLUS
DOCUMENT NUMBER:          134:306172
TITLE:                    Corynebacterium thermoaminogenes genes for enzymes
                          involved in amino acid biosynthesis,
                          recombinant expression for L-amino
                          acid biosynthesis
INVENTOR(S):              Hirano, Seiko; Nonaka, Gen; Matsuzaki, Yumi; Akiyoshi,
                          Naoki; Nakamura, Kanae; Kimura, Eiichiro; Osumi,
                          Tsuyoshi; Matsui, Kazuhiko; Kawahara, Yoshio;
                          Kurahashi, Osamu; Nakamatsu, Tsuyoshi; Sugimoto,
                          Shinichi
PATENT ASSIGNEE(S):       Ajinomoto Co., Inc., Japan
SOURCE:                   PCT Int. Appl., 215 pp.
                          CODEN: PIXXD2
DOCUMENT TYPE:            Patent
```

LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001025447	A1	20010412	WO 2000-JP6913	20001004
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
AU 2000075561	A5	20010510	AU 2000-75561	20001004
EP 1219712	A1	20020703	EP 2000-964654	20001004
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL				
BR 2000014496	A	20020820	BR 2000-14496	20001004

PRIORITY APPLN. INFO.:
JP 1999-282716 A 19991004
JP 1999-311147 A 19991101
JP 2000-120687 A 20000421
WO 2000-JP6913 W 20001004

AB Genes for enzymes involved in amino acid biosynthesis from thermophilic bacterium Corynebacterium thermoaminogenes, and **recombinant expression** of those genes in microorganisms for L-amino acid biosynthesis, are disclosed. Those enzymes showed enhanced thermal stability compared to the corresponding enzymes from Corynebacterium glutamicum. The isocitrate lyase gene, aceA, was **cloned** and sequenced. Acetyl CoA carboxylase (ACC) subunit encoding accBC operon was **cloned**. DtsR1 and dtsR2 genes were also **cloned** and sequenced. A gene (pfk) coding for 6-phosphofructokinase was **cloned**. ScrB gene encoding a sucrose 6-phosphate specific invertase, and indispensable for sucrose (Scr) utilization, was **cloned**. A 4-gene cluster (gluABCD) assocd. with glutamate uptake was **cloned**. The genes pdhA, encoding the E1 subunits of the pyruvate dehydrogenase (PDH) E1 component, was **cloned**. A gene (pc) for pyruvate carboxylase, an important anaplerotic enzyme replenishing oxaloacetate consumed for biosynthesis during growth, or lysine and glutamic acid prodn. in industrial fermns., was **cloned**. The ppc gene, which encodes phosphoenolpyruvate carboxylase (PEPC), was **cloned** and sequenced. The aconitase [9024-25-3] gene (acn) was **cloned**. Sequence of the icd gene, encoding isocitrate dehydrogenase (IDH), was obtained. Dihydrolipoamide dehydrogenase (LPD) apoprotein gene (lpd) was identified, sequenced and analyzed. OdhA gene, encoding 2-oxoglutarate dehydrogenase was **cloned**. A gene coding for glutamate dehydrogenase (gdh) was **cloned**. Nucleotide sequence was obtained for the citrate synthase encoding gene (gltA).

REFERENCE COUNT: 96 THERE ARE 96 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 2 OF 31 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2001:31660 HCAPLUS
DOCUMENT NUMBER: 134:96288
TITLE: Brevibacterium lactofermentum gene ptsIIsuc, encoding enzyme II of the sucrose phosphoenolpyruvate-dependent phosphotransferase system
INVENTOR(S): Izui, Masako; Sugimoto, Masakazu; Nakamatsu, Tsuyoshi; Kurahashi, Osamu
PATENT ASSIGNEE(S): Ajinomoto Co., Inc., Japan
SOURCE: PCT Int. Appl., 45 pp.
CODEN: PIXXD2

DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001002584	A1	20010111	WO 2000-JP4348	20000630
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
EP 1197555	A1	20020417	EP 2000-940903	20000630
R: BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
BR 2000012020	A	20020702	BR 2000-12020	20000630

PRIORITY APPLN. INFO.: JP 1999-189512 A 19990702
WO 2000-JP4348 W 20000630

AB A Brevibacterium lactofermentum gene, designated ptsIIsuc, encoding a protein with homol. to enzyme IIScr of the phosphoenolpyruvate-dependent sucrose phosphtransferase system (PTS) and encoded enzyme, are disclosed. The gene was **cloned** from Brevibacterium lactofermentum AJ12036 and sequenced. A strain of Brevibacterium lactofermentum with disruption in ptsIIsuc gene was constructed and it showed inability to grow in culture medium having sucrose as the only carbon source.

REFERENCE COUNT: 15 THERE ARE 15 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 3 OF 31 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 2001:796329 HCAPLUS
DOCUMENT NUMBER: 135:314432
TITLE: Transformed Escherichia coli containing **sucrose phosphotransferase** system (PTS) and non-PTS genes, and their use in production of amino acids utilizing sucrose
INVENTOR(S): Livshits, Vitaliy Arkadyevich; Doroshenko, Vera Georgievna; Mashko, Sergei Vladimirovich; Akhverdian, Valery Zavenovich; Kozlov, Yuri Ivanovich
PATENT ASSIGNEE(S): Ajinomoto Co., Ltd., Japan
SOURCE: Eur. Pat. Appl., 17 pp.
CODEN: EPXXDW
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
EP 1149911	A2	20011031	EP 2001-109779	20010420
EP 1149911	A3	20020403		
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
JP 2001346578	A2	20011218	JP 2001-117409	20010416
US 2001049126	A1	20011206	US 2001-841609	20010425

PRIORITY APPLN. INFO.: RU 2000-110350 A 20000426

AB The invention provides **recombinant** Escherichia coli contg. **sucrose phosphotransferase** system (PTS) genes (scr) or non-PTS genes (csc). The invention relates that the non-PTS csc genes encode proton symport transport system (LacY type permease), invertase or

fructokinase. The invention also provides the use of said transformed E. coli in the prodn. of amino acids, such as threonine, homoserine, isoleucine, lysine, valine and tryptophan, utilizing sucrose. The invention related that the collection and purifn. of amino acids from the liq. medium may be performed in a manner similar to the conventional fermn. method.

L4 ANSWER 4 OF 31 MEDLINE DUPLICATE 1
ACCESSION NUMBER: 2001563402 MEDLINE
DOCUMENT NUMBER: 21521406 PubMed ID: 11640984
TITLE: Modeling of inducer exclusion and catabolite repression based on a PTS-dependent sucrose and non-PTS-dependent glycerol transport systems in Escherichia coli K-12 and its experimental verification.
AUTHOR: Wang J; Gilles E D; Lengeler J W; Jahreis K
CORPORATE SOURCE: Institut fur Systemdynamik und Regelungstechnik, Pfaffenwaldring 9, 70550 Stuttgart, Germany.. wang@isr.uni-stuttgart.de
SOURCE: JOURNAL OF BIOTECHNOLOGY, (2001 Dec 28) 92 (2) 133-58. Journal code: 8411927. ISSN: 0168-1656.
PUB. COUNTRY: Netherlands
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200202
ENTRY DATE: Entered STN: 20011022
Last Updated on STN: 20020226
Entered Medline: 20020225

AB We used genetically engineered sucrose positive Escherichia coli K-12 derivatives as a model system for the modeling and experimental verification of regulatory processes in bacteria. These cells take up and metabolize sucrose by the phosphoenolpyruvate (PEP)-dependent **sucrose phosphotransferase** system (Scr-PTS). **Expression** of the scr genes, which cluster in two different operons (scrYAB and scrK), is negatively controlled by the ScrR repressor. Additionally, **expression** of the scrYAB operon, but not of the scrK operon is positively controlled by the cAMP-CRP complex. Modeling of sucrose transport and metabolism through the Scr-system and of the scr gene **expression** has been performed using a modular and object-orientated new approach. To verify the model and identify important model parameters we measured in a first set of experiments induction kinetics of the scr genes after growth on glycerol using strains with single copy lacZ operon fusions in the scrK or scrY genes, respectively. In a second set of experiments an additional copy of the complete scr-regulon was integrated into the chromosome to construct diplogenotic strains. Differences were observed in the induction kinetics of the cAMP-CRP-dependent scrY operon compared to the cAMP-CRP independent scrK operon as well as between the single copy and the corresponding diplogenotic strains.

L4 ANSWER 5 OF 31 MEDLINE
ACCESSION NUMBER: 2001010944 MEDLINE
DOCUMENT NUMBER: 20444180 PubMed ID: 10986236
TITLE: Molecular analysis of sucrose metabolism of Erwinia amylovora and influence on bacterial virulence.
AUTHOR: Bogs J; Geider K
CORPORATE SOURCE: Max-Planck-Institut fur Zellbiologie, Rosenhof, D-68526 Ladenburg, Germany.
SOURCE: JOURNAL OF BACTERIOLOGY, (2000 Oct) 182 (19) 5351-8. Journal code: 2985120R. ISSN: 0021-9193.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals

ENTRY MONTH: 200010
ENTRY DATE: Entered STN: 20010322
Last Updated on STN: 20010322
Entered Medline: 20001024

AB Sucrose is an important storage and transport sugar of plants and an energy source for many phytopathogenic bacteria. To analyze regulation and biochemistry of sucrose metabolism of the fire blight pathogen Erwinia amylovora, a chromosomal fragment which enabled Escherichia coli to utilize sucrose as sole carbon source was **cloned**. By transposon mutagenesis, the scr regulon of E. amylovora was tagged, and its nucleotide sequence was determined. Five open reading frames, with the genes scrK, scrY, scrA, scrB, and scrR, had high homology to genes of the scr regulons from Klebsiella pneumoniae and plasmid pUR400. scrB and scrR of E. amylovora were fused to a histidine tag and to the maltose-binding protein (MalE) of E. coli, respectively. ScrB (53 kDa) catalyzed the hydrolysis of sucrose with a K(m) of 125 mM. Binding of a MalE-ScrR fusion protein to an scrYAB promoter fragment was shown by gel mobility shifts. This complex dissociated in the presence of fructose but not after addition of sucrose. **Expression** of the scr regulon was studied with an scrYAB promoter-green fluorescent protein gene fusion and measured by flow cytometry and spectrofluorometry. The operon was affected by catabolite repression and induced by sucrose or fructose. The level of gene induction correlated to the sucrose concentration in plant tissue, as shown by flow cytometry. Sucrose mutants created by site-directed mutagenesis did not produce significant fire blight symptoms on apple seedlings, indicating the importance of sucrose metabolism for colonization of host plants by E. amylovora.

L4 ANSWER 6 OF 31 MEDLINE
ACCESSION NUMBER: 1999337080 MEDLINE
DOCUMENT NUMBER: 99337080 PubMed ID: 10411273
TITLE: The genes controlling sucrose utilization in Clostridium beijerinckii NCIMB 8052 constitute an operon.
AUTHOR: Reid S J; Rafudeen M S; Leat N G
CORPORATE SOURCE: Department of Microbiology, University of Cape Town, Rondebosch, South Africa.. shez@molbiol.uct.ac.za
SOURCE: MICROBIOLOGY, (1999 Jun) 145 (Pt 6) 1461-72.
Journal code: 9430468. ISSN: 1350-0872.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-AF059741
ENTRY MONTH: 199908
ENTRY DATE: Entered STN: 19990913
Last Updated on STN: 19990913
Entered Medline: 19990830

AB The sucrose operon of Clostridium beijerinckii NCIMB 8052 comprises four genes, which encode a sucrose-specific enzyme IIBC(Scr) protein of the phosphotransferase system (ScrA), a transcriptional repressor (ScrR), a sucrose hydrolase (ScrB) and an ATP-dependent fructokinase (ScrK). The scrARBK operon was **cloned** in Escherichia coli in three stages. Initial isolation was achieved by screening a C. beijerinckii genomic library in E. coli for **clones** able to utilize sucrose, while the remainder of the operon was isolated by inverse PCR and by plasmid rescue of flanking regions from a scrB mutant constructed by targeted gene disruption. Substrate specificity assays confirmed that the sucrose hydrolase was a beta-fructofuranosidase, able to hydrolyse sucrose and raffinose but not inulin or levans, and that the scrK gene encoded an ATP/Mg2+-dependent fructokinase. Both enzyme activities were induced by sucrose in C. beijerinckii. Disruption of the scr operon of C. beijerinckii by targeted plasmid integration into either the scrR or the scrB gene resulted in strains unable to utilize sucrose, indicating that this was the only inducible sucrose catabolic pathway in this organism.

RNA analysis confirmed that the genes of the scr operon were co-transcribed on a 5 kb mRNA transcript and that transcription was induced by sucrose, but not by glucose, fructose, maltose or xylose. Primer extension experiments identified the transcriptional start site as lying 44 bp upstream of the scrA ATG start codon, immediately adjacent to the imperfect pelindrome sequence proposed to be a repressor binding site. Disruption of the scrR gene resulted in constitutive transcription of the upstream scrA gene, suggesting that ScrR encodes a transcriptional repressor which acts at the scrA operator sequence. The scrR gene is therefore itself negatively autoregulated as part of the polycistronic scrARBK mRNA

L4 ANSWER 7 OF 31 MEDLINE DUPLICATE 2
ACCESSION NUMBER: 2000082965 MEDLINE
DOCUMENT NUMBER: 20082965 PubMed ID: 10613841
TITLE: Regulation of the alpha-galactosidase activity in Streptococcus pneumoniae: characterization of the raffinose utilization system.
AUTHOR: Rosenow C; Maniar M; Trias J
CORPORATE SOURCE: Versicor, Inc., Fremont, California 94555, USA.. carsten_rosenow@affymetrix.com
SOURCE: GENOME RESEARCH, (1999 Dec) 9 (12) 1189-97. Journal code: 9518021. ISSN: 1088-9051.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 200001
ENTRY DATE: Entered STN: 20000204
Last Updated on STN: 20000204
Entered Medline: 20000127

AB A 10.2-kb gene region was identified in the Streptococcus pneumoniae genome sequence that contains eight genes involved in regulation and metabolism of raffinose. The genes rafR and rafS are transcribed as one operon, and their gene products regulate the raffinose-dependent stimulation of a divergently transcribed second promoter (P(A)) directing the **expression** of aga, the structural gene for alpha-galactosidase. Raffinose-mediated transcription from P(A) results in a 500-fold increase in alpha-galactosidase activity in the cell. A third promoter within the cluster is responsible for the transcription of the remaining five genes (rafE, rafF, rafG, gtfA, and rafX), whose gene products might be involved in transport and metabolism of raffinose. The presence of additional internal promoters cannot be excluded. The aga promoter P(A) is negatively regulated by the presence of sucrose in the growth medium. Consistent with catabolite repression (CR), a DNA sequence with high homology to the CRE (cis-active element) was identified upstream of the aga promoter. Sucrose-mediated CR depends on the phosphoenolpyruvate: **sucrose phosphotransferase** system (PTS) but is unaffected by a mutation in a gene encoding a homolog of the CRE regulatory protein CcpA.

L4 ANSWER 8 OF 31 SCISEARCH COPYRIGHT 2002 ISI (R) DUPLICATE 3
ACCESSION NUMBER: 1998:590868 SCISEARCH
THE GENUINE ARTICLE: 103TJ
TITLE: Regulation of sucrose-6-phosphate hydrolase activity in Streptococcus mutans: Characterization of the scrR gene
AUTHOR: Hiratsuka K; Wang B; Sato Y; Kuramitsu H (Reprint)
CORPORATE SOURCE: SUNY ALBANY, DEPT ORAL BIOL, 3435 MAIN ST, BUFFALO, NY 14214 (Reprint); SUNY ALBANY, DEPT ORAL BIOL, BUFFALO, NY 14214
COUNTRY OF AUTHOR: USA
SOURCE: INFECTION AND IMMUNITY, (AUG 1998) Vol. 66, No. 8, pp. 3736-3743.
Publisher: AMER SOC MICROBIOLOGY, 1325 MASSACHUSETTS

AVENUE, NW, WASHINGTON, DC 20005-4171.
ISSN: 0019-9567.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: English
REFERENCE COUNT: 38
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB Previous results have implicated an important role for the enzyme IIScr, the sucrose-specific permease, in the transport of sucrose by cariogenic Streptococcus mutans, The product of the scrB gene, sucrose-6-phosphate hydrolase (Suc-6PH), is required for the metabolism of phosphorylated sucrose, The results from the utilization of scrB::lacZ fusions in S. mutans GS-5 have suggested that sucrose-grown cells have higher levels of scrB gene **expression** than do cells grown with glucose or fructose, Northern blot analysis of scrB transcripts has also confirmed the relative strengths of **expression** as sucrose>glucose>fructose, Immediately downstream from the scrB gene, an open reading frame with homology to regulatory proteins of the GalR-LacI family as well as to ScrR proteins from several other bacteria has been identified. In addition, this gene appears to be transcribed in the same operon as scrB, Inactivation of this gene, scrR, did not alter the relative **expression** of the scrB gene in the presence of sucrose or fructose but did increase SUC-6PH levels in the presence of glucose to that observed with sucrose, Furthermore, the S, mutans ScrR homolog appears to bind to the scrB promoter region as determined from the results of gel shift assays. These results suggest that the scrR gene is involved in the regulation of scrB, and likely scrA, **expression**. However, it is not clear whether sucrose acts as an inducer of **expression** of these genes or, alternatively, whether glucose and fructose act as repressors.

L4 ANSWER 9 OF 31 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1997:504765 HCAPLUS
DOCUMENT NUMBER: 127:215761
TITLE: Gene organization and regulatory sequences in the sucrose utilization cluster of Bacillus stearothermophilus NUB36
AUTHOR(S): Li, Yang; Ferenci, Thomas
CORPORATE SOURCE: Department of Microbiology G08, University of Sydney, Sydney, Australia
SOURCE: Gene (1997), 195(2), 195-200
CODEN: GENED6; ISSN: 0378-1119
PUBLISHER: Elsevier
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The nucleotide sequence of the surP and surT genes in a sucrose-utilization cluster **cloned** from Bacillus stearothermophilus NUB36 was detd. The surP gene encoded a protein of 466 amino acid residues and shared 60-62% amino acid identity with the sucrose-specific enzyme II components of the phosphotransferase system of Bacillus subtilis, Salmonella typhimurium and Klebsiella pneumoniae. SurP, like other sucrose EIIs, lacked the hydrophilic domain contg. the first (IIA) phosphorylation site. The surT gene encoded a 278 amino acid polypeptide which showed 63.1% and 54% amino acid identity to the B. subtilis antiterminators SacT and SacY, resp. A region contg. a palindromic structure preceding surP was highly homologous to the regulatory transcription termination regions of the sacPA and sacB operons of B. subtilis and the bgl operon of Escherichia coli. Hence the sucrose gene cluster of B. stearothermophilus NUB36 is very similar to the B. subtilis sacPA operon in terms of gene order and regulatory organization.

L4 ANSWER 10 OF 31 MEDLINE DUPLICATE 4
ACCESSION NUMBER: 96188840 MEDLINE
DOCUMENT NUMBER: 96188840 PubMed ID: 8628219

TITLE: Molecular analysis of the scrA and scrB genes from Klebsiella pneumoniae and plasmid pUR400, which encode the sucrose transport protein Enzyme II Scr of the phosphotransferase system and a sucrose-6-phosphate invertase.
AUTHOR: Titgemeyer F; Jahreis K; Ebner R; Lengeler J W
CORPORATE SOURCE: University of Groningen, Department of Biochemistry, The Netherlands.
SOURCE: MOLECULAR AND GENERAL GENETICS, (1996 Feb 5) 250 (2) 197-206.
Journal code: 0125036. ISSN: 0026-8925.
PUB. COUNTRY: GERMANY: Germany, Federal Republic of
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-L06761; GENBANK-M22711; GENBANK-M33761; GENBANK-M76768; GENBANK-X57401; GENBANK-X67750; GENBANK-X69800
ENTRY MONTH: 199606
ENTRY DATE: Entered STN: 19960708
Last Updated on STN: 19980206
Entered Medline: 19960621

AB The Klebsiella pneumoniae genes scrA and scrB are indispensable for sucrose (Scr) utilisation. Gene scrA codes for an Enzyme IIScr (IIScr) transport protein of the phosphoenolpyruvate-dependent carbohydrate: phosphotransferase system (PTS), while scrB encodes a sucrose 6-phosphate specific invertase. A 3.7 kbscr AB DNA fragment has been **cloned** from K. pneumoniae and **expressed** in Escherichia coli. Its nucleotide sequence was determined and the coding regions for scrA (1371 bp) and scrB (1401 bp) were identified by genetic complementation, enzyme activity test and radiolabelling of the gene products. In addition, the nucleotide sequence of the scrB gene from conjugative plasmid pUR400 isolated from Salmonella typhimurium was also determined and errors in the previously published sequence of the scrA gene of pUR400 were corrected. Extensive similarity was found between the sequences of ScrA and other Enzymes II, as well as between the two invertases and other sucrose hydrolysing enzymes. Based on the analysis of seven IIScr proteins, a hypothetical model of the secondary structure of IIScr is proposed.

L4 ANSWER 11 OF 31 MEDLINE DUPLICATE 5
ACCESSION NUMBER: 95394807 MEDLINE
DOCUMENT NUMBER: 95394807 PubMed ID: 7665480
TITLE: Use of a novel mobilizable vector to inactivate the scrA gene of Streptococcus sobrinus by allelic replacement.
AUTHOR: Buckley N D; Lee L N; LeBlanc D J
CORPORATE SOURCE: University of Texas Health Science Center at San Antonio 78284-7758, USA.
CONTRACT NUMBER: DE08915 (NIDCR)
SOURCE: JOURNAL OF BACTERIOLOGY, (1995 Sep) 177 (17) 5028-34.
Journal code: 2985120R. ISSN: 0021-9193.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199510
ENTRY DATE: Entered STN: 19951020
Last Updated on STN: 20000303
Entered Medline: 19951011

AB The virulence factors of the cariogenic bacterium Streptococcus sobrinus have been difficult to assess because of a lack of tools for the genetic manipulation of this organism. The construction of an Escherichia coli-Streptococcus shuttle vector, pDL289, that can be mobilized into S. sobrinus by the conjugative plasmid pAM beta 1 was described in a previous report. The vector contains pVA380-1 for replication and mobilization in

streptococci, the pSC101 replicon for maintenance in E. coli, a kanamycin resistance marker that functions in both hosts, and the multiple **cloning** site and lacZ from pGEM7Zf(-). pDL289 is stable with or without selection in several species of Streptococcus. In this study, a derivative with a deletion in the minus origin of the pVA380-1 component of pDL289 was constructed. This derivative, pDL289 delta 202, was less stable than pDL289 in Streptococcus gordonii Challis, Streptococcus mutans, and S. sobrinus. Both pDL289 and pDL289 delta 202 were mobilizable by pAM beta 1 into S. sobrinus, with frequencies of 3 x 10(-6) and 1 x 10(-7) transconjugants per recipient CFU, respectively. The **cloned** scrA gene of S. sobrinus 6715-10 coding for the EIISuc of the sucrose-specific phosphoenolpyruvate phosphotransferase system was interrupted by the insertion of a streptococcal spectinomycin resistance gene active in E. coli and streptococci. The interrupted scrA gene was subcloned into both pDL289 and pDL289 delta 202. Each **recombinant** plasmid was introduced into the DL1 strain of S. gordonii Challis, which was then used as a recipient for the conjugative transfer of pAM beta 1.(ABSTRACT TRUNCATED AT 250 WORDS)

L4 ANSWER 12 OF 31 MEDLINE
ACCESSION NUMBER: 95332210 MEDLINE
DOCUMENT NUMBER: 95332210 PubMed ID: 7608078
TITLE: Molecular analysis of treB encoding the Escherichia coli enzyme II specific for trehalose.
AUTHOR: Klein W; Horlacher R; Boos W
CORPORATE SOURCE: Department of Biology, University of Konstanz, Germany.
SOURCE: JOURNAL OF BACTERIOLOGY, (1995 Jul) 177 (14) 4043-52. Journal code: 2985120R. ISSN: 0021-9193.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-U06195; SWISSPROT-P36672
ENTRY MONTH: 199508
ENTRY DATE: Entered STN: 19950828
Last Updated on STN: 19950828
Entered Medline: 19950815

AB A gene bank of partially Sau3A-digested Escherichia coli DNA ligated in plasmid pBR322 was screened for the ability to complement a mutant unable to metabolize trehalose at low osmolarity. The resulting plasmid was shown to contain the genes encoding transport (treB) and metabolic (treC) functions. The complementing DNA region was sequenced and shown to contain an operon of two genes, with treB as the promoter proximal gene and with treC as the promoter distal gene. The transcriptional start point was determined, and one major transcript was detected. The control region of the operon was found to contain consensus binding motifs for the cyclic AMP-catabolite activator protein complex and for a specific repressor protein whose gene, treR, is located immediately upstream of treB, being transcribed in the same direction as treB treC. The products of both genes could be **expressed** in minicells in which TreB revealed itself as a protein with an apparent molecular weight of 42,000. The gene product of treB consists of 485 amino acids with a calculated molecular weight of 52,308. It showed high homology to enzymes IIScr of enteric bacteria specific for the uptake of sucrose and encoded by plasmid pUR400 of enteric bacteria. Like enzyme IIScr, enzyme IITre belongs to the EIIBC domain type and lacks a covalently bound EIIA domain. Instead, enzyme IITre-mediated phosphorylation of trehalose requires the activity of enzyme IIAGlc, a component of the major glucose transport system.

L4 ANSWER 13 OF 31 SCISEARCH COPYRIGHT 2002 ISI (R)
ACCESSION NUMBER: 95:347326 SCISEARCH
THE GENUINE ARTICLE: QX752
TITLE: PURIFICATION AND CHARACTERIZATION OF THE PHOSPHO-ALPHA(1,1)GLUCOSIDASE (TREA) OF

BACILLUS-SUBTILIS-168
AUTHOR: GOTSCHE S; DAHL M K (Reprint)
CORPORATE SOURCE: UNIV ERLANGEN NURNBERG, INST MIKROBIOL BIOCHEM & GENET, LEHRSTUHL MIKROBIOL, STAUDTSTR 5, D-91058 ERLANGEN, GERMANY (Reprint); UNIV ERLANGEN NURNBERG, INST MIKROBIOL BIOCHEM & GENET, LEHRSTUHL MIKROBIOL, D-91058 ERLANGEN, GERMANY
COUNTRY OF AUTHOR: GERMANY
SOURCE: JOURNAL OF BACTERIOLOGY, (MAY 1995) Vol. 177, No. 10, pp. 2721-2726.
ISSN: 0021-9193.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: ENGLISH
REFERENCE COUNT: 47

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB The intracellular phospho-alpha(1,1)glucosidase TreA from Bacillus subtilis has been overproduced in Escherichia coli and purified by ion-exchange chromatography and gel filtration, The molecular mass, estimated by sodium dodecyl sulfate-polyacrylamide gel electrophoresis, was 64 kDa, Isoelectric focusing indicated homogeneity of the protein, and its pi was determined to be 4.3. Characterization of the enzyme showed a protein which is stable up to 44 degrees C after temperature treatment for 15 min, The temperature optimum was found to be 37 degrees C, and the pH optimum was 4.5, TreA activity is stimulated by high salt concentrations with different efficiencies depending on the kind of salt. When increasing amounts of ammonium sulfate are used, the increase of TreA activity is correlated with a conformational change of the protein or dimerization, The substrate specificity of the purified enzyme was characterized, showing additionally that trehalose is also hydrolyzed, but to a much smaller extent than trehalose-6-phosphate. In vitro, the presence of glucose reduces TreA activity, indicating product inhibition of the enzyme.

L4 ANSWER 14 OF 31 SCISEARCH COPYRIGHT 2002 ISI (R)
ACCESSION NUMBER: 95:293504 SCISEARCH
THE GENUINE ARTICLE: QU564
TITLE: CLEAVAGE OF TREHALOSE-PHOSPHATE IN BACILLUS-SUBTILIS IS CATALYZED BY A PHOSPHO-ALPHA-(1-1)-GLUCOSIDASE ENCODED BY THE TREA GENE
AUTHOR: HELFERT C; GOTSCHE S; DAHL M K (Reprint)
CORPORATE SOURCE: UNIV ERLANGEN NURNBERG, INST MIKROBIOL BIOCHEM & GENET, LEHRSTUHL MIKROBIOL, STAUDTSTR 5, D-91058 ERLANGEN, GERMANY (Reprint); UNIV ERLANGEN NURNBERG, INST MIKROBIOL BIOCHEM & GENET, LEHRSTUHL MIKROBIOL, D-91058 ERLANGEN, GERMANY
COUNTRY OF AUTHOR: GERMANY
SOURCE: MOLECULAR MICROBIOLOGY, (APR 1995) Vol. 16, No. 1, pp. 111-120.
ISSN: 0950-382X.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: ENGLISH
REFERENCE COUNT: 50

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB A 2.5 kb DNA fragment contain a gene encoding a phospho-alpha-(1-1)-glucosidase (phosphotrehalase), designated treA, was isolated from a Bacillus subtilis chromosomal library by complementation of the tre-12 mutation. The major TreA activity was found in the cytoplasm. TreA exhibits high sequence similarity to thermostable oligo 1,6 beta-glucosidases of several species and the trehalose-6-phosphate hydrolase TreC of Escherichia coli. TreA activity is induced by trehalose and repressed by glucose, fructose or mannitol. Induction by trehalose and repression by glucose are concentration dependent. The highest activity of

TreA occurs 90 min before the end of the exponential growth phase in crude cell extracts. The enzyme is able to cleave para-nitrophenylglucopyranoside and trehalose-6-phosphate but not trehalose. These results indicate that treA encodes a specific phospho-alpha-(1-1)-glucosidase which cleaves trehalose-6-phosphate in the cytoplasm after transport and phosphorylation of trehalose. The 5' flanking region of treA contains an open reading frame which was partially sequenced, whose product shows about 40% identity to sucrose Enzyme II of the phosphotransferase transport system from several organisms.

L4 ANSWER 15 OF 31 SCISEARCH COPYRIGHT 2002 ISI (R)
ACCESSION NUMBER: 94:213369 SCISEARCH
THE GENUINE ARTICLE: NC074
TITLE: GENETIC-REGULATION OF FRUCTOSYLTRANSFERASE IN STREPTOCOCCUS-MUTANS
AUTHOR: KISKA D L; MACRINA F L (Reprint)
CORPORATE SOURCE: POB 980678 MCV, RICHMOND, VA, 23298 (Reprint); VIRGINIA COMMONWEALTH UNIV, DEPT MICROBIOL & IMMUNOL, RICHMOND, VA, 23298
COUNTRY OF AUTHOR: USA
SOURCE: INFECTION AND IMMUNITY, (APR 1994) Vol. 62, No. 4, pp. 1241-1251.
ISSN: 0019-9567.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: ENGLISH
REFERENCE COUNT: 55
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB Streptococcus mutans possesses several extracellular sucrose-metabolizing enzymes which have been implicated as important virulence factors in dental caries. This study was initiated to investigate the genetic regulation of one of these enzymes, the extracellular fructosyltransferase (Ftf). Fusions were constructed with the region upstream of the S. mutans GS5 Ftf gene (ftf) and a promoterless chloramphenicol acetyltransferase (CAT) gene. The fusions were integrated at a remote site in the chromosome, and transcriptional activity in response to the addition of various carbohydrates to the growth medium was measured. A significant increase in CAT activity was observed when glucose-groan cells were shifted to sucrose-containing medium. Sucrose-induced **expression** was repressed immediately upon addition of phosphoenolpyruvate phosphotransferase system sugars to the growth media. Deletion analysis of the ftf upstream region revealed that an inverted repeat structure was involved in the control of ftf **expression** in response to carbohydrate. However, the control of the level of ftf transcription appeared to involve a region distinct from that mediating carbohydrate regulation. CAT gene fusions also were constructed with the ftf upstream region from S. mutans V403, a fructan-hyperproducing strain which synthesizes increased levels of Ftf. Sequence analysis of the upstream ftf region in this strain revealed several nucleotide sequence changes which were associated with high-level ftf **expression**. Comparison of the GS5 and V403 ftf **expression** patterns suggested the presence of a trans-acting factor(s) involved in modulation of ftf **expression** in response to carbohydrate. This factor(s) was either absent or altered in V403, resulting in the inability of this organism to respond to the presence of carbohydrate. The sequences of the ftf regions from three additional fructan-hyperproducing strains were determined and compared with that of V403. Only one strain displayed nucleotide changes similar to those of V403. Two additional strains did not have these changes, suggesting that several mechanisms for up-regulation of ftf **expression** exist.

L4 ANSWER 16 OF 31 SCISEARCH COPYRIGHT 2002 ISI (R)
ACCESSION NUMBER: 93:355111 SCISEARCH
THE GENUINE ARTICLE: LE498

TITLE: SEQUENCE-ANALYSIS OF SCRA AND SCRB FROM STREPTOCOCCUS-SOBRINUS 6715
AUTHOR: CHEN Y Y M; LEE L N; LEBLANC D J (Reprint)
CORPORATE SOURCE: UNIV TEXAS, HLTH SCI CTR, DEPT MICROBIOL, 7703 FLOYD CURL DR, SAN ANTONIO, TX, 78284
COUNTRY OF AUTHOR: USA
SOURCE: INFECTION AND IMMUNITY, (JUN 1993) Vol. 61, No. 6, pp. 2602-2610.
ISSN: 0019-9567.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: ENGLISH
REFERENCE COUNT: 50

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB The complete nucleotide sequences of Streptococcus sobrinus 6715 scrA and scrB, which encode sucrose-specific enzyme II of the phosphoenolpyruvate-dependent phosphotransferase system and sucrose-6-phosphate hydrolase, respectively, have been determined. These two genes were transcribed divergently, and the initiation codons of the two open reading frames were 192 bp apart. The transcriptional initiation sites were determined by primer extension analysis, and the putative promoter regions of these two genes overlapped partially. The gene encoding enzyme II(Scr), scrA, contained 1,896 nucleotides, and the molecular mass of the predicted protein was 66,529 Da. The hydropathy plot of the predicted amino acid sequence indicated that enzyme II(Scr) was a relatively hydrophobic protein. The gene encoding sucrose-6-phosphate hydrolase, scrB, contained 1,437 nucleotides. The molecular mass of the predicted protein was 54,501 Da, and the encoded enzyme was hydrophilic. The predicted amino acid sequences of the two open reading frames exhibited approximately 45 and 70% identity with those encoded by scrA and scrB, respectively, from Streptococcus mutans GS5. Homology also was observed between-the N-terminal region of the S. sobrinus 6715 enzyme II(Scr) and other enzyme IIs specific for the glucopyranoside molecule, all of which generate glucopyranoside-6-phosphate during translocation and phosphorylation of the respective substrates. The sequence of the C-terminal domain of the S. sobrinus 6715 enzyme II(Scr) shared significant homology with enzyme III(Glc) from Escherichia coli and Salmonella typhimurium and with the C-terminal domain of enzyme II(Glc) from E. coli, indicating that the two functional domains, enzyme II(Src) and enzyme III(Src), were covalently linked as a single polypeptide in S. sobrinus 6715. The deduced amino acid sequence of the gene product of S. sobrinus scrB shared strong homology with sucrase from Bacillus subtilis, Klebsiella pneumoniae, and Vibrio alginolyticus, suggesting conservation based on the physiological roles of these proteins.

L4 ANSWER 17 OF 31 SCISEARCH COPYRIGHT 2002 ISI (R)
ACCESSION NUMBER: 93:336844 SCISEARCH
THE GENUINE ARTICLE: LD452
TITLE: ISOLATION, CHARACTERIZATION AND SEQUENCE-ANALYSIS OF THE SCRK GENE ENCODING FRUCTOKINASE OF STREPTOCOCCUS-MUTANS
AUTHOR: SATO Y (Reprint); YAMAMOTO Y; KIZAKI H; KURAMITSU H K
CORPORATE SOURCE: TOKYO DENT COLL, DEPT BIOCHEM, 2-2 MASAGO 1 CHOME, MIHAMA KU, CHIBA 261, JAPAN (Reprint); UNIV TEXAS, HLTH SCI CTR, DEPT PEDIAT DENT, SAN ANTONIO, TX, 78284
COUNTRY OF AUTHOR: JAPAN; USA
SOURCE: JOURNAL OF GENERAL MICROBIOLOGY, (MAY 1993) Vol. 139, Part 5, pp. 921-927.
ISSN: 0022-1287.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: ENGLISH
REFERENCE COUNT: 28

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB A gene encoding an ATP-dependent fructokinase from Streptococcus mutans

GS-5 was identified within a 2 kb DNA fragment immediately downstream from the scrA gene. The gene **cloned** in Escherichia coli also **expressed** mannokinase activity. Insertional inactivation of this gene in S. mutans markedly decreased both fructokinase and mannokinase activities. Nucleotide sequence analysis of the 2 kb fragment revealed an ORF starting 199 bp downstream from the scrA gene, preceded by potential ribosome-binding (Shine-Dalgarno) and promoter-like sequences. This ORF specified a putative protein of 293 amino acids with a calculated M(r) of 31681. The deduced amino acid sequence of the fructokinase gene, scrK, from S. mutans exhibited no significant similarity to fructokinase genes from Klebsiella pneumoniae, E. coli plasmid pUR400 or Vibrio alginolyticus, but was similar to a comparable gene from Zymomonas mobilis.

L4 ANSWER 18 OF 31 SCISEARCH COPYRIGHT 2002 ISI (R) DUPLICATE 6
ACCESSION NUMBER: 93:68990 SCISEARCH
THE GENUINE ARTICLE: KJ739
TITLE: CHROMOSOME ORGANIZATION OF STREPTOCOCCUS-MUTANS GS-5
AUTHOR: HANTMAN M J; SUN S Z; PIGGOT P J; DANEOMOORE L (Reprint)
CORPORATE SOURCE: TEMPLE UNIV, HLTH SCI CTR, SCH MED, DEPT MICROBIOL & IMMUNOL, PHILADELPHIA, PA, 19140
COUNTRY OF AUTHOR: USA
SOURCE: JOURNAL OF GENERAL MICROBIOLOGY, (JAN 1993) Vol. 139, Part 1, pp. 67-77.
ISSN: 0022-1287.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: ENGLISH
REFERENCE COUNT: 57
ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB Twenty-eight genetic loci have been physically mapped to specific large restriction fragments of the Streptococcus mutans GS-5 chromosome by hybridization with probes of **cloned** genes or, for transposon-generated amino acid auxotrophs, with probes for Tn916. In addition, restriction fragments generated by one low-frequency-cleavage enzyme were used as probes to identify overlapping fragments generated by other restriction enzymes. The approach allowed construction of a low resolution physical map of the S. mutans GS-5 genome using restriction enzymes ApaI (5'-GGGCC/C), SmaI (5'-CCC/GGG), and NotI (5'-GC/GGCCGC).

L4 ANSWER 19 OF 31 MEDLINE DUPLICATE 7
ACCESSION NUMBER: 94049686 MEDLINE
DOCUMENT NUMBER: 94049686 PubMed ID: 8232209
TITLE: **Cloning** and characterization of the scrA gene encoding the sucrose-specific Enzyme II of the phosphotransferase system from Staphylococcus xylosus.
AUTHOR: Wagner E; Gotz F; Bruckner R
CORPORATE SOURCE: Mikrobielle Genetik, Universitat Tubingen, Germany.
SOURCE: MOLECULAR AND GENERAL GENETICS, (1993 Oct) 241 (1-2) 33-41.
Journal code: 0125036. ISSN: 0026-8925.
PUB. COUNTRY: GERMANY: Germany, Federal Republic of
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-X69800
ENTRY MONTH: 199312
ENTRY DATE: Entered STN: 19940117
Last Updated on STN: 19940117
Entered Medline: 19931215

AB By insertional mutagenesis with the staphylococcal transposon Tn551, mutants of Staphylococcus xylosus were isolated that were unable to utilize sucrose. One of these was found to be deficient in sucrose uptake. The genomic region containing this sucrose uptake gene of Staphylococcus xylosus (scrA) was **cloned** in Staphylococcus carnosus. The scrA

gene was further localized to a 4.4 kb DNA fragment by complementation of the sucrose transport-deficient S. xylosus mutant. The DNA sequence analysis of the scrA region revealed three open reading frames, one of which encodes a protein of 480 amino acids (51.335 kDa) with significant similarity to sucrose-specific Enzymes II of phosphoenolpyruvate-dependent carbohydrate phosphotransferase systems (PTS). A protein with an apparent molecular weight of 50 kDa was obtained in Escherichia coli by **expression** of scrA with the bacteriophage T7 RNA polymerase promoter system. Transcriptional start sites of the scrA gene were localized by primer extension analysis to positions 46 and 49 nucleotides upstream of the scrA start codon. No additional sucrose utilization genes are encoded close to scrA on the S. xylosus chromosome.

L4 ANSWER 20 OF 31 MEDLINE DUPLICATE 8
ACCESSION NUMBER: 92363573 MEDLINE
DOCUMENT NUMBER: 92363573 PubMed ID: 1500184
TITLE: Genetic analysis of scrA and scrB from Streptococcus sobrinus 6715.
AUTHOR: Chen Y Y; LeBlanc D J
CORPORATE SOURCE: Department of Microbiology, University of Texas Health Science Center, San Antonio 78284-7758.
CONTRACT NUMBER: DE08915 (NIDCR)
SOURCE: INFECTION AND IMMUNITY, (1992 Sep) 60 (9) 3739-46. Journal code: 0246127. ISSN: 0019-9567.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199209
ENTRY DATE: Entered STN: 19920925
Last Updated on STN: 20000303
Entered Medline: 19920917

AB A DNA fragment containing scrA and scrB, which encode enzyme II of the phosphoenolpyruvate-dependent **sucrose phosphotransferase** system and sucrose-6-phosphate hydrolase, respectively, was isolated from a lambda gt10 genomic DNA library of Streptococcus sobrinus 6715. Both genes were located on a 4.2-kb DNA fragment which was maintained stably in Escherchia coli on low-copy-number vector pGB2. The **recombinant** E. coli **clone expressed** sucrose-hydrolytic activity on MacConkey agar base supplemented with raffinose or sucrose. Results from deletion analysis showed that the sucrose-metabolic activity was contained within a 3.5-kb region. The lactic acid bacterium Lactococcus lactis subsp. lactis LM0230, which is devoid of sucrose-metabolic activity, was used to study the enzyme activities encoded by scrA and scrB from S. sobrinus 6715. L. lactis transformants carrying the 4.2-kb S. sobrinus-derived DNA fragment on E. coli-Streptococcus shuttle vector pDL278 were able to grow at the expense of sucrose and exhibited enzyme II and sucrose-6-phosphate hydrolase activities. Results from hybridization studies and a comparison of the restriction endonuclease maps of the scrA- and scrB-containing chromosomal regions from S. mutans GS5 and S. sobrinus 6715 suggested considerable divergence.

L4 ANSWER 21 OF 31 MEDLINE
ACCESSION NUMBER: 93062804 MEDLINE
DOCUMENT NUMBER: 93062804 PubMed ID: 1435727
TITLE: Characterization of a chromosomally encoded, non-PTS metabolic pathway for sucrose utilization in Escherichia coli EC3132.
AUTHOR: Bockmann J; Heuel H; Lengeler J W
CORPORATE SOURCE: Universitat Osnabruck, Fachbereich Biologie/Chemie, FRG.
SOURCE: MOLECULAR AND GENERAL GENETICS, (1992 Oct) 235 (1) 22-32. Journal code: 0125036. ISSN: 0026-8925.
PUB. COUNTRY: GERMANY: Germany, Federal Republic of
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-X63740
ENTRY MONTH: 199212
ENTRY DATE: Entered STN: 19930122
Last Updated on STN: 19930122
Entered Medline: 19921208

AB A wild-type isolate, EC3132, of Escherichia coli, that is able to grow on sucrose was isolated and its csc genes (mnemonic for chromosomally coded sucrose genes) transferred to strains of E. coli K12. EC3132 and all sucrose-positive exconjugants and transductants invariably showed a D-serine deaminase (Dsd)-negative phenotype. The csc locus maps adjacent to dsdA, the structural gene for the D-serine deaminase, and contains an inducible regulon, controlled by a sucrose-specific repressor CscR, together with structural genes for a sucrose hydrolase (invertase) CscA, for a D-fructokinase CscK, and for a transport system CscB. Based on DNA sequencing studies, this last codes for a hydrophobic protein of 415 amino acids. CscB is closely related to the beta-galactoside transport system LacY (31.2% identical residues) and a raffinose transport system RafB (32.3% identical residues) of the enteric bacteria, both of the proton symport type. A two-dimensional model common to the three transport proteins, which is based on the integrated consensus sequence, will be discussed.

L4 ANSWER 22 OF 31 MEDLINE DUPLICATE 9
ACCESSION NUMBER: 91169631 MEDLINE
DOCUMENT NUMBER: 91169631 PubMed ID: 2004831
TITLE: Repeated DNA sequence involved in mutations affecting transport of sucrose into Streptococcus mutans V403 via the phosphoenolpyruvate phosphotransferase system.
AUTHOR: Macrina F L; Jones K R; Alpert C A; Chassy B M; Michalek S M
CORPORATE SOURCE: Department of Microbiology and Immunology, Virginia Commonwealth University, Richmond 23298-0678.
CONTRACT NUMBER: DE04224 (NIDCR)
DE08182 (NIDCR)
DE09035 (NIDCR)
SOURCE: INFECTION AND IMMUNITY, (1991 Apr) 59 (4) 1535-43.
Journal code: 0246127. ISSN: 0019-9567.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199104
ENTRY DATE: Entered STN: 19910512
Last Updated on STN: 20000303
Entered Medline: 19910425

AB Mutants of Streptococcus mutans V403 defective in the intracellular sucrose-6-phosphate hydrolase (product of the scrB gene) are sensitive to sucrose because of the intracellular accumulation of the phosphorylated sugar. Using a scrB mutant prepared by allelic exchange, we have isolated and characterized a number of sucrose-resistant revertants. One such mutant was found to lack the ability to transport sucrose into the cell via the phosphoenolpyruvate-dependent **sucrose phosphotransferase** system (PTS). Genetic analysis of this strain revealed this lesion to be linked to the scrB gene. This was corroborated by the physical demonstration of an insertion mutation very near scrB. Taken together with DNA sequence information (Y. Sato, F. Poy, G. R. Jacobson, and H. K. Kuramitsu, J. Bacteriol. 171:263-271, 1989), our results indicated that all of the mutations characterized were located in the adjoining scrA gene which encodes the membrane-associated, sugar-specific enzyme II (EIIsucrose) component of the sucrose PTS in S. mutans. Biochemically, such a genetic lesion disables the sucrose PTS and prevents sucrose from entering the cell by this system. In this paper, we

detail the nature of two independent insertion mutations and conclude them to be the result of duplicative transposition events into the scrA gene. This region of the chromosome was amplified and purified in large quantities by using the polymerase chain reaction. Examination of the amplified DNA revealed that the two independent insertion mutations were composed of sequences that were indistinguishable by size and by restriction site endonuclease maps. Their insertion points in the scrA gene were approximately 200 bp apart. The amplified DNA fragment was also used as a probe to demonstrate the presence of five copies of this element on the S. mutans V403 chromosome. A second strain, S. mutans V310, also was found to carry similarly arranged, multiple copies of this sequence on its chromosome, suggesting a **clonal** origin of V403 and V310. The small size of this sequence, its presence in multiple copies on the V403 chromosome, and its ability to duplicate itself semiconservatively into remote sites argue compellingly that it is an insertion sequence element. One such insertion mutant, with a defective sucrose PTS, was tested for virulence in rats and was found to cause caries at levels similar to those of the wild-type strain.

L4 ANSWER 23 OF 31 SCISEARCH COPYRIGHT 2002 ISI (R)
ACCESSION NUMBER: 91:47654 SCISEARCH
THE GENUINE ARTICLE: ET446
TITLE: PLASMID-MEDIATED SUCROSE METABOLISM IN ESCHERICHIA-COLI - CHARACTERIZATION OF SCRY, THE STRUCTURAL GENE FOR A PHOSPHOENOLPYRUVATE-DEPENDENT **SUCROSE PHOSPHOTRANSFERASE** SYSTEM OUTER-MEMBRANE PORIN
AUTHOR: HARDESTY C; FERRAN C; DIRIENZO J M (Reprint)
CORPORATE SOURCE: UNIV PENN, SCH DENT MED, DEPT MICROBIOL, PHILADELPHIA, PA, 19104
COUNTRY OF AUTHOR: USA
SOURCE: JOURNAL OF BACTERIOLOGY, (1991) Vol. 173, No. 2, pp. 449-456.
DOCUMENT TYPE: Article; Journal
FILE SEGMENT: LIFE
LANGUAGE: ENGLISH
REFERENCE COUNT: 40

ABSTRACT IS AVAILABLE IN THE ALL AND IALL FORMATS

AB The scrY gene, part of the pUR400-borne sucrose regulon, appeared to be transcribed from its own promoter, with the transcriptional start site located 58 bp upstream from the initiation codon. An open reading frame encoding a polypeptide of 505 amino acid residues (M(r) 55,408) was identified. The first 22 amino acid residues formed a leader sequence typical to those found in other procaryotic outer membrane and periplasmic proteins. A frameshift mutation in the scrY gene resulted in a dramatic decrease in sucrose transport with no effect on in vitro phosphorylation activity associated with enzyme II(scr). The rate of diffusion of sucrose was 96 times greater than the rate of diffusion of lactose or maltose in liposomes containing the ScrY protein. This increase in sucrose permeability provided strong evidence that the ScrY protein functions as a sucrose porin. There was 23% amino acid sequence identify between the ScrY protein and LamB, a maltose proin from Escherichia coli.

L4 ANSWER 24 OF 31 MEDLINE
ACCESSION NUMBER: 91285381 MEDLINE
DOCUMENT NUMBER: 91285381 PubMed ID: 1905660
TITLE: Construction of scrA::lacZ gene fusions to investigate regulation of the sucrose PTS of Streptococcus mutans.
AUTHOR: Sato Y; Yamamoto Y; Suzuki R; Kizaki H; Kuramitsu H K
CORPORATE SOURCE: Department of Biochemistry, Tokyo Dental College, Chiba, Japan.
CONTRACT NUMBER: DE-03258 (NIDCR)
SOURCE: FEMS MICROBIOLOGY LETTERS, (1991 Apr 15) 63 (2-3) 339-45. Journal code: 7705721. ISSN: 0378-1097.
PUB. COUNTRY: Netherlands

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 199108
ENTRY DATE: Entered STN: 19910825
Last Updated on STN: 20000303
Entered Medline: 19910805

AB The scrA gene coding for sucrose EnzymeII of the phosphoenolpyruvate dependent phosphotransferase system previously isolated from Streptococcus mutans was fused in vitro to the promoterless lacZ' gene to monitor the **expression** of the scrA gene. The scrA::lacZ gene fusion was introduced back into S. mutans GS-5IS3 by two independent transformation procedures involving either linear or plasmid DNA to produce both scrA and scrA+ mutants. These mutants should prove useful for analyzing the regulation of sucrose transport in S. mutans.

L4 ANSWER 25 OF 31 LIFESCI COPYRIGHT 2002 CSA
ACCESSION NUMBER: 90:70485 LIFESCI
TITLE: What is the role of levansucrase in Bacillus subtilis ?. PROCEEDINGS OF THE INTERNATIONAL CONFERENCE ON THE MECHANISMS BETWEEN SOIL-PLANT-MICROORGANISMS IN THE RHIZOSPHERE.
AUTHOR: Aymerich, S.
CORPORATE SOURCE: Lab. Genet., IN APG, F-78850 Thiverval-Grignon, France
SOURCE: SYMBIOSIS., (1990) pp. 179-184.
Meeting Info.: International Conference on the Mechanisms of the Relationship between Soil-Plant-Microorganisms in the Rhizosphere. Montpellier (France). 28-29 Sep 1989.
DOCUMENT TYPE: Book
TREATMENT CODE: Conference
FILE SEGMENT: J; G
LANGUAGE: English
SUMMARY LANGUAGE: English

AB B. subtilis possesses two metabolic pathways for sucrose and a complex constellation of regulators involved in the control of their **expression**. The constellation includes genes which are involved in the induction by sucrose of saccharolytic enzymes and the deg genes which have pleiotropic effects. The function of both these sets of regulators is beginning to be understood but the reasons of this complexity are unknown. A speculative interpretation is proposed.

L4 ANSWER 26 OF 31 MEDLINE DUPLICATE 10
ACCESSION NUMBER: 89123027 MEDLINE
DOCUMENT NUMBER: 89123027 PubMed ID: 2536656
TITLE: Characterization and sequence analysis of the scrA gene encoding enzyme IIScr of the Streptococcus mutans phosphoenolpyruvate-dependent **sucrose phosphotransferase** system.
AUTHOR: Sato Y; Poy F; Jacobson G R; Kuramitsu H K
CORPORATE SOURCE: Department of Microbiology-Immunology, Northwestern University Medical-Dental Schools, Chicago, Illinois 60611.
CONTRACT NUMBER: DE-03258 (NIDCR)
DE-05966 (NIDCR)
SOURCE: JOURNAL OF BACTERIOLOGY, (1989 Jan) 171 (1) 263-71.
Journal code: 2985120R. ISSN: 0021-9193.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-M22711
ENTRY MONTH: 198903
ENTRY DATE: Entered STN: 19900308
Last Updated on STN: 20000303
Entered Medline: 19890313

AB The Streptococcus mutans GS-5 scrA gene coding for enzyme IIScr of the phosphoenolpyruvate-dependent **sucrose phosphotransferase** system (PTS) was localized upstream from the scrB gene coding for sucrose-6-phosphate hydrolase activity after Mu dE transposon mutagenesis of plasmid pMH613. The **cloned** scrA gene product was identified as a 68-kilodalton protein by minicell analysis after isolation of the gene in plasmid pD4. In addition, the membrane fraction from Escherichia coli cells containing pD4 exhibited sucrose PTS activity upon complementation with enzyme I and HPr from strain GS-5. The nucleotide sequence of the scrA region revealed that this gene was located immediately upstream from the scrB gene and divergently transcribed from the opposite DNA strand. The scrA gene was preceded by potential Shine-Dalgarno and promoterlike sequences and was followed by a transcription terminator-like sequence. The scrA gene coded for an enzyme IIScr protein of 664 amino acid residues with a calculated molecular weight of 69,983. This enzyme IIScr protein was larger than the comparable proteins from Bacillus subtilis and E. coli containing sucrose-metabolizing plasmid pUR400. The 491-amino-acid N-terminal sequence of the S. mutans enzyme IIScr was homologous with the B. subtilis and E. coli sequences, and the 173-amino-acid C-terminal sequence of the S. mutans protein was also homologous with the Salmonella typhimurium enzyme IIIGlc and the 162-amino-acid C terminus of E. coli enzyme IIBgl. These results suggest that the sucrose PTS system of S. mutans is enzyme III independent.

L4 ANSWER 27 OF 31 MEDLINE
ACCESSION NUMBER: 88216186 MEDLINE
DOCUMENT NUMBER: 88216186 PubMed ID: 3285123
TITLE: DNA sequence of the gene scrA encoding the sucrose transport protein EnzymeII(Scr) of the phosphotransferase system from enteric bacteria: homology of the EnzymeII(Scr) and EnzymeII(Bgl) proteins.
AUTHOR: Ebner R; Lengeler J W
CORPORATE SOURCE: Fachbereich Biologie/Chemie, Universitat Osnabruck, FRG.
SOURCE: MOLECULAR MICROBIOLOGY, (1988 Jan) 2 (1) 9-17.
Journal code: 8712028. ISSN: 0950-382X.
PUB. COUNTRY: ENGLAND: United Kingdom
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198806
ENTRY DATE: Entered STN: 19900308
Last Updated on STN: 19900308
Entered Medline: 19880614

AB The nucleotide sequence of the structural gene, scrA, which codes for sucrose-specific EnzymeII(Scr) (EII(Scr)) of the phosphoenolpyruvate-dependent carbohydrate:phosphotransferase system (PTS), was determined. EIIScr requires an EnzymeIII, the product of the gene crr, for full activity. The gene scrA is preceded immediately by a classical Shine-Dalgarno sequence (AAGAGGGTA). It contains 1368 nucleotides with an increased GC-content (58%) corresponding to a polypeptide of 455 amino acid residues (Mr 47,500). The protein has the hydropathic profile (average hydropathy +0.82) of an integral membrane protein lacking extended alpha-helical structures and a signal peptide. Comparison with the sequence of the beta-glucoside-specific EnzymeII (EII(Bgl), 625 amino acids, Mr 66,480; Bramley and Kornberg, 1987a; Schnetz et al., 1987) revealed strong homologies between EiI(Scr) and the first 458 residues of EII(Bgl). The 162 carboxyterminal residues of EII(Bgl), however, showed a high homology with the sequence of EnzymeIII (Nelson et al., 1984), a homology also described recently by Bramley and Kornberg (1987b). The evolutionary and functional significance of the similarities with four other EnzymesII is discussed.

L4 ANSWER 28 OF 31 MEDLINE DUPLICATE 11

ACCESSION NUMBER: 88097369 MEDLINE
DOCUMENT NUMBER: 88097369 PubMed ID: 3122206
TITLE: Bacillus subtilis sucrose-specific enzyme II of the phosphotransferase system: **expression** in Escherichia coli and homology to enzymes II from enteric bacteria.
AUTHOR: Fouet A; Arnaud M; Klier A; Rapoport G
CORPORATE SOURCE: Unite de Biochimie Microbienne, Departement des Biotechnologies, Institut Pasteur, Paris, France.
SOURCE: PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA, (1987 Dec) 84 (24) 8773-7. Journal code: 7505876. ISSN: 0027-8424.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
OTHER SOURCE: GENBANK-J03006
ENTRY MONTH: 198802
ENTRY DATE: Entered STN: 19900305
Last Updated on STN: 19900305
Entered Medline: 19880220

AB Sucrose is transported into Bacillus subtilis cells by way of a phosphotransferase system, which consists of a specific enzyme II, a nonspecific enzyme I, and a histidine-containing phosphocarrier protein. Mutations in the sacP locus abolish the specific transport of sucrose. The B. subtilis sacP gene was **cloned** and **expressed** in Escherichia coli, and transformed cells could transport and phosphorylate sucrose. This indicates that the sacP gene product is enzyme II of the **sucrose phosphotransferase** system of B. subtilis. The nucleotide sequence of the sacP gene was determined and was found to overlap with the sacA gene at the tetranucleotide ATGA, which may allow a translational coupling between sacP and sacA. The two genes are therefore probably organized in an operon structure with the promoter located 5' to sacP gene. The deduced amino acid sequence gave a Mr of 48,945 for the sucrose-specific enzyme II polypeptide. The amino acid sequence was compared to that of three other known enteric bacterial enzymes II (beta-glucoside-specific enzyme II, mannitol-specific enzyme II, and glucose-specific enzyme II). Homology was found with beta-glucoside enzyme II, and well conserved regions were identified through the comparison of the proteins.

L4 ANSWER 29 OF 31 MEDLINE DUPLICATE 12
ACCESSION NUMBER: 86195827 MEDLINE
DOCUMENT NUMBER: 86195827 PubMed ID: 3009399
TITLE: Molecular **cloning** and characterization of scrB, the structural gene for the Streptococcus mutans phosphoenolpyruvate-dependent **sucrose phosphotransferase** system sucrose-6-phosphate hydrolase.
AUTHOR: Lunsford R D; Macrina F L
CONTRACT NUMBER: DE04224 (NIDCR)
SOURCE: JOURNAL OF BACTERIOLOGY, (1986 May) 166 (2) 426-34. Journal code: 2985120R. ISSN: 0021-9193.
PUB. COUNTRY: United States
DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)
LANGUAGE: English
FILE SEGMENT: Priority Journals
ENTRY MONTH: 198606
ENTRY DATE: Entered STN: 19900321
Last Updated on STN: 20000303
Entered Medline: 19860620

AB A DNA fragment encoding the sucrose-6-phosphate hydrolase component of the Streptococcus mutans phosphoenolpyruvate-dependent **sucrose phosphotransferase** system has been recovered from a plasmid-based

genomic library of strain GS5. The locus, designated scrB, was found to reside within a 2.9-kilobase-pair restriction fragment present on the chimeric molecule pVA1343 (7.3 kilobase pairs). Minicell analysis of pVA1343-directed translation products revealed that the scrB product synthesized in Escherichia coli V1343 was a single peptide of Mr 57,000. This polypeptide was reactive with antiserum prepared against S. mutans intracellular invertase, which has been previously shown to have an Mr of 43,000 to 48,000. The basis of this difference in Mr was not established but may represent a posttranslational proteolytic event which occurred in S. mutans but not in **recombinant** V1343. Sucrose-6-phosphate hydrolase purified to homogeneity from V1343 exhibited Michaelis constants of 180 mM for sucrose and 0.08 mM for sucrose-6-phosphate. Deletion analysis of pVA1343 facilitated the assignment of a coding region for the hydrolase within the insert, as well as an orientation for the transcription of scrB. scrB-defective strains of S. mutans constructed by additive integration of an insertionally inactivated scrB locus exhibited the sucrose sensitivity characteristic of this mutant class. Similar loci were detected by DNA-DNA hybridization in additional strains of S. mutans and two strains of Streptococcus cricetus, but not in single strain representatives of S. rattus, S. sobrinus, S. sanguis I and II, S. salivarius, or S. mitis.

L4 ANSWER 30 OF 31 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1986:492419 HCAPLUS
DOCUMENT NUMBER: 105:92419
TITLE: Genetic and biochemical analysis of **cloned** sucrase determinants from Streptococcus mutans
AUTHOR(S): Macrina, Francis L.; Pucci, Michael J.; Lundsford, R. Dwayne
CORPORATE SOURCE: Dep. Microbiol. Immunol., Virginia Commonw. Univ., Richmond, VA, 23298, USA
SOURCE: Mol. Microbiol. Immunobiol. Streptococcus Mutans, Proc. Int. Conf. "Cell., Mol. Clin. Aspects Streptococcus Mutans" (1986), Meeting Date 1985, 181-9. Editor(s): Hamada, Shigeyuki. Elsevier: Amsterdam, Neth.
CODEN: 55CZAF
DOCUMENT TYPE: Conference
LANGUAGE: English
AB Two different sucrase [37288-39-4] determinants of S. mutans were **cloned** in Escherichia coli and functionally characterized. The gtfA gene may be involved in H2O-insol. glucan synthesis, based on its behavior in S. sanguis strains. The scrB gene encodes a sucrase with a very high affinity for sucrase 6-phosphate and is likely the hydrolase that works in concert with the S. mutans **sucrose phosphotransferase** uptake system. Both gtfA and scrB are conserved in S. mutans strains that cause dental caries in humans.

L4 ANSWER 31 OF 31 HCAPLUS COPYRIGHT 2002 ACS
ACCESSION NUMBER: 1981:529040 HCAPLUS
DOCUMENT NUMBER: 95:129040
TITLE: Uptake and metabolism of sucrose by Streptococcus lactis
AUTHOR(S): Thompson, John; Chassy, Bruce M.
CORPORATE SOURCE: New Zealand Dairy Res. Inst., Palmerston North, N. Z.
SOURCE: J. Bacteriol. (1981), 147(2), 543-51
CODEN: JOBAAY; ISSN: 0021-9193
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Transport and metab. of sucrose in S. lactis K1 were examd. Starved cells of S. lactis K1 grown previously on sucrose accumulated [14C]sucrose by a phosphoenolpyruvate-dependent **phosphotransferase** (**sucrose**-PTS) system. The product of group translocation was sucrose 6-phosphate. A specific sucrose 6-phosphate hydrolase was

identified which cleaved the disaccharide phosphate to glucose 6-phosphate and fructose. Exts. prepd. from sucrose-grown cells also contained an ATP-dependent mannofructokinase which catalyzed the conversion of fructose to fructose 6-phosphate (Km, 0.33 mM). The sucrose-PTS and sucrose 6-phosphate hydrolase activities were coordinately induced during growth on sucrose. Mannofructokinase appeared to be regulated independently of the sucrose-PTS and sucrose 6-phosphate hydrolase, since **expression** also occurred when S. lactis K1 was grown on non-PTS sugars. **Expression** of the mannofructokinase may be neg. regulated by a component (or a deriv.) of the PTS.

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SFIELDS at an arrow prompt (=>).

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E2           42     POMPEIUS R/AU
E3           28 --> POMPEJUS M/AU
E4           26     POMPEJUS MARKUS/AU
E5           37     POMPEKIRN V/AU
E6            1     POMPEL M/AU
E7            1     POMPEL P/AU
E8            1     POMPELEAN A/AU
E9            1     POMPELIA D MICK/AU
E10           2     POMPELIA DONALD M/AU
E11           2     POMPELIANO O/AU
E12         224     POMPELLA A/AU

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L5           28 "POMPEJUS M"/AU

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L2       5695523 S CLON? OR EXPRESS? OR RECOMBINANT
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L4            31 DUP REM L3 (33 DUPLICATES REMOVED)
                 E POMPEJUS M/AU
L5            28 S E3

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L6            0 L4 AND L5

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E5          749     SCHRODER H C/AU
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E10           1      SCHRODER H DAA/AU
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                 E SCHRODER H/AU
L7          1962 S E3

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L7          1962 S E3
L8             0 S L4 AND L7

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E12           1      KROGER C S/AU

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L9           93 "KROGER B"/AU
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L9             93 S E3
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